

# How to use MRICloud

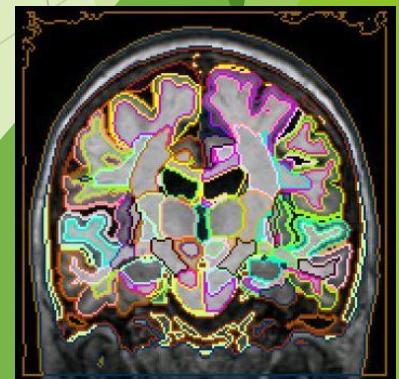
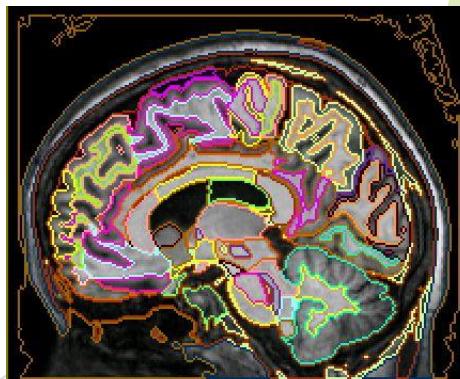
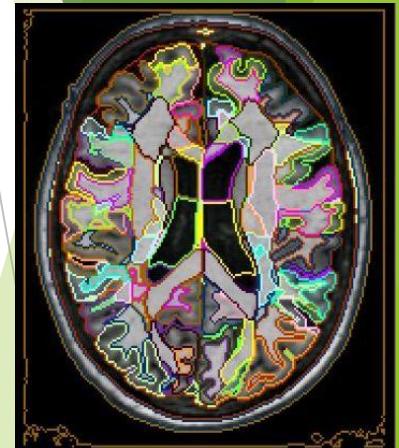
## T1 MultiAtlas Segmentation

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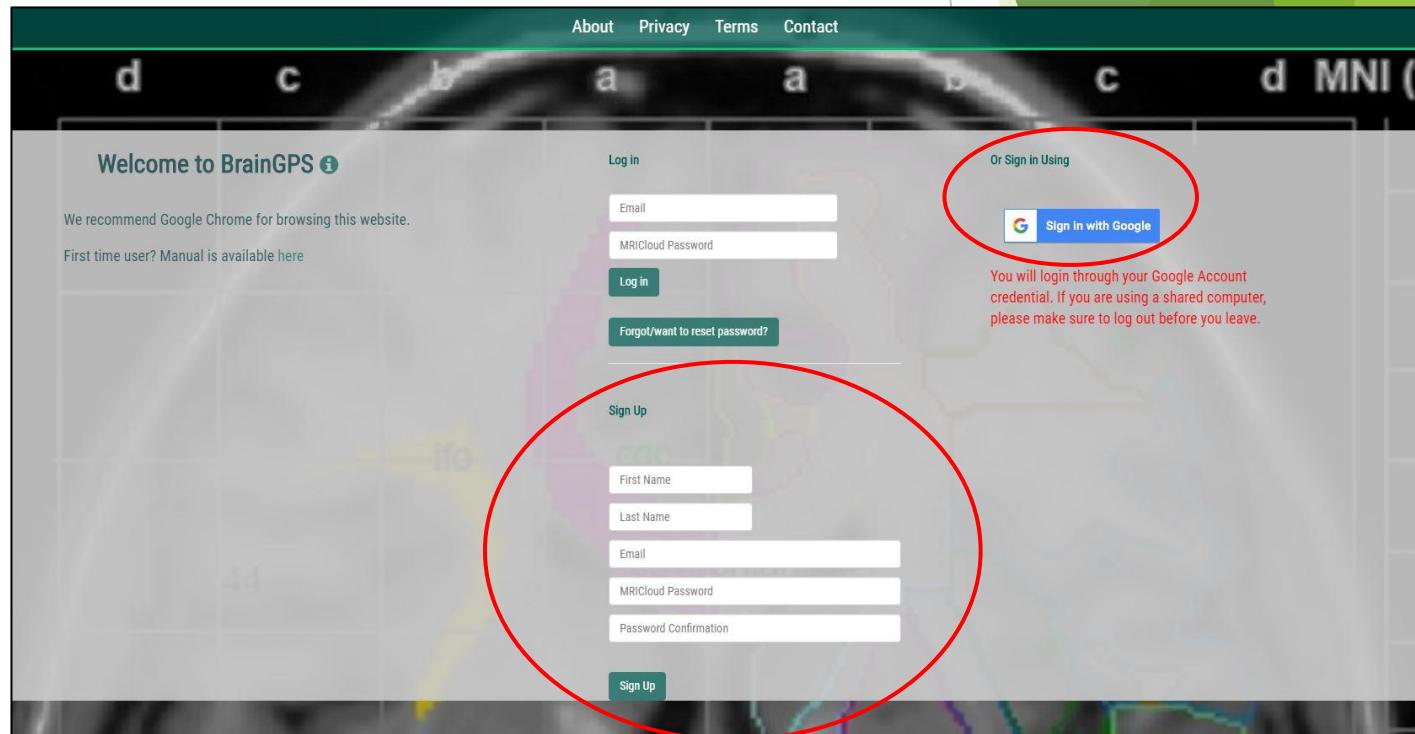
# Purpose and Overview

- ▶ To segment T1 brain images and find the volumes of various brain structures
- ▶ MriCloud provides automated brain parcellation, or segmentation, of T1 (MPRAGE) images
  
- ▶ What you need: Dicom images from scanner (not from PACS or other data archiving system) or Analyze image that you can verify left-right orientation\*
- \*more detail on slide 6
  
- ▶ Basic flow of the T1 pipeline after preparing and submitting Analyze data:
  - ❖ Submit Analyze image >> image linearly normalized to MNI space >> normalized MNI image segmented with labeling >> segmentation images linearly back-transferred to native space
  
- ▶ Output of T1 pipeline:
  - ❖ Native Analyze image + its segmentation images
  - ❖ MNI image + its segmentation images
  - ❖ Summary volume text files of Native and MNI segmentation



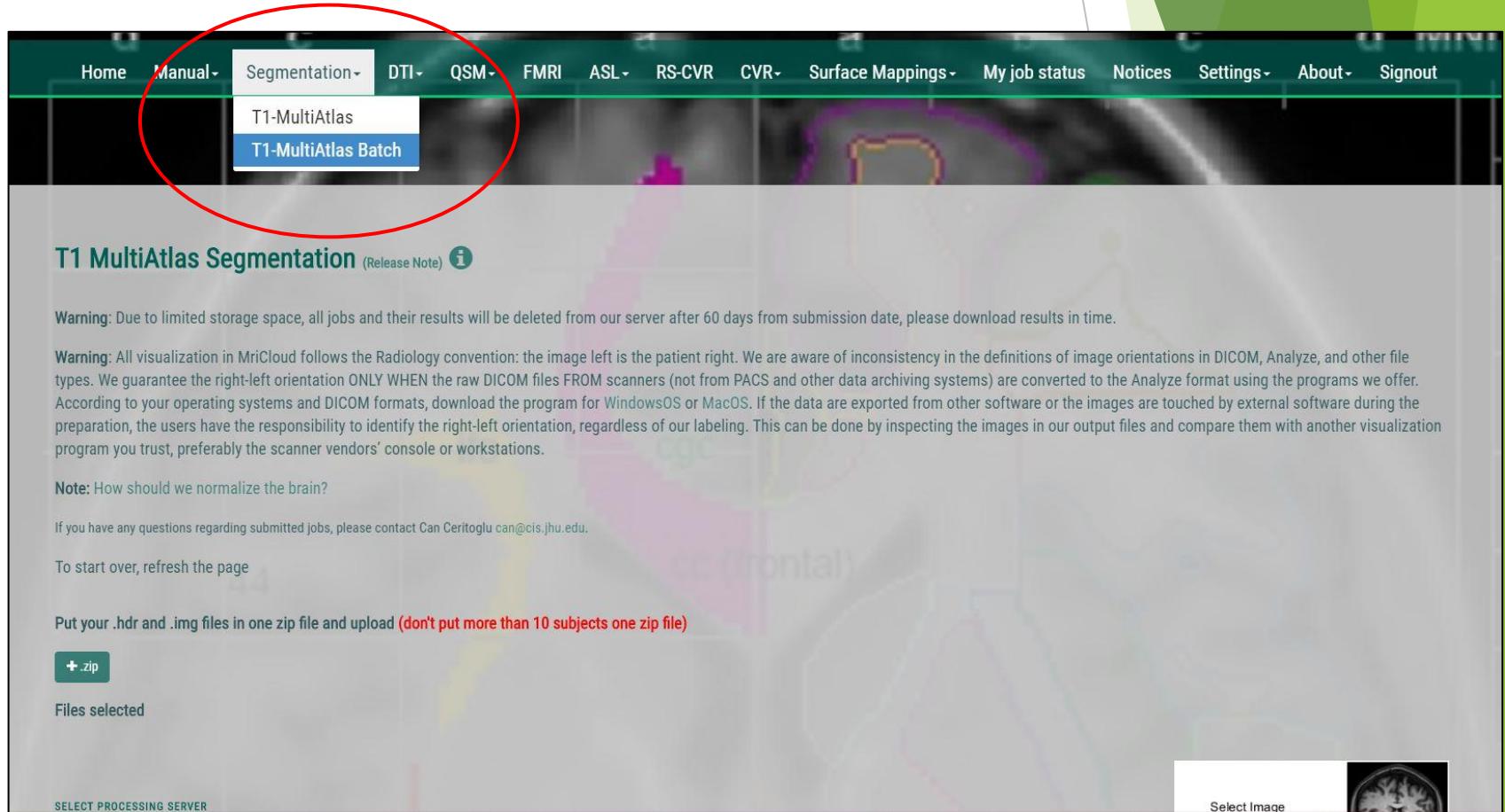
# MriCloud - Login

- ▶ Go to <https://braingps.mricloud.org>
  - Use of Google chrome browser is recommended
- ▶ First-time users can either sign up for an MriCloud account, or use their existing Google account to sign in



# MriCloud - T1 Batch

- Once signed in, go to Segmentation >> T1-MultiAtlas Batch



The screenshot shows the MriCloud web application interface. At the top, there is a navigation bar with various links: Home, Manual, Segmentation (which is currently selected and highlighted in blue), DTI, QSM, FMRI, ASL, RS-CVR, CVR, Surface Mappings, My job status, Notices, Settings, About, and Signout. A red circle highlights the 'Segmentation' dropdown menu, which is open to show two options: 'T1-MultiAtlas' and 'T1-MultiAtlas Batch'. Below the navigation bar, the main content area has a header 'T1 MultiAtlas Segmentation' with a '(Release Note)' link and an information icon. It contains several warning and note sections. A large image of a brain with colored overlays (red, green, blue) is visible in the background. At the bottom, there is a file upload section with a button '+ .zip' and a placeholder text 'Files selected'. A 'SELECT PROCESSING SERVER' button is at the very bottom.

**T1 MultiAtlas Segmentation** (Release Note) ⓘ

**Warning:** Due to limited storage space, all jobs and their results will be deleted from our server after 60 days from submission date, please download results in time.

**Warning:** All visualization in MriCloud follows the Radiology convention: the image left is the patient right. We are aware of inconsistency in the definitions of image orientations in DICOM, Analyze, and other file types. We guarantee the right-left orientation ONLY WHEN the raw DICOM files FROM scanners (not from PACS and other data archiving systems) are converted to the Analyze format using the programs we offer. According to your operating systems and DICOM formats, download the program for WindowsOS or MacOS. If the data are exported from other software or the images are touched by external software during the preparation, the users have the responsibility to identify the right-left orientation, regardless of our labeling. This can be done by inspecting the images in our output files and compare them with another visualization program you trust, preferably the scanner vendors' console or workstations.

**Note:** How should we normalize the brain?

If you have any questions regarding submitted jobs, please contact Can Ceritoglu [can@cis.jhu.edu](mailto:can@cis.jhu.edu).

To start over, refresh the page

Put your .hdr and .img files in one zip file and upload **(don't put more than 10 subjects one zip file)**

+ .zip

Files selected

SELECT PROCESSING SERVER

Select Image

# Analyze Image - Dcm2Analyze software

- ▶ First, Dicom files must be converted to Analyze image. Download our Dicom-to-Analyze converter from T1 MultiAtlas Segmentation page.
  - ▶ Click on either WindowsOS or MacOS (see yellow arrows on the image) to download Dcm2Analyze software

\*We follow **Radiology convention**, and can guarantee right-left (R-L) image orientation and its matching R-L segmentation labeling **ONLY WHEN** the raw Dicom files from scanners are converted to the Analyze format using our Dcm2Analze converter.

\*\*If user prefer to use images that are not directly from scanners or that have gone through external software during preparation, the user has the responsibility to confirm R-L orientation of the output image, regardless of our R-L labeling, using another visualization program you can trust.

**T1 MultiAtlas Segmentation** (Release Note) 

**Warning:** Due to limited storage space, all jobs and their results will be deleted from our server after 60 days from submission date, please download results in time.

**Warning:** All visualization in MriCloud follows the Radiology convention: the image left is the patient right. We are aware of inconsistency in the definitions of image orientations in DICOM, Analyze, and other file types. We guarantee the right-left orientation ONLY WHEN the raw DICOM files FROM scanners (not from PACS and other data archiving systems) are converted to the Analyze format using the programs we offer. According to your operating systems and DICOM formats, download the program for [WindowsOS](#) or [MacOS](#). If the data are exported from other software or the images are touched by external software during the preparation, the users have the responsibility to identify the right-left orientation, regardless of our labeling. This can be done by inspecting the images in our output files and compare them with another visualization program you trust, preferably the scanner vendors' console or workstations.

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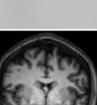
To start over, refresh the page

Put your .hdr and .img files in one zip file and upload **(don't put more than 10 subjects one zip file)**

 + .zip

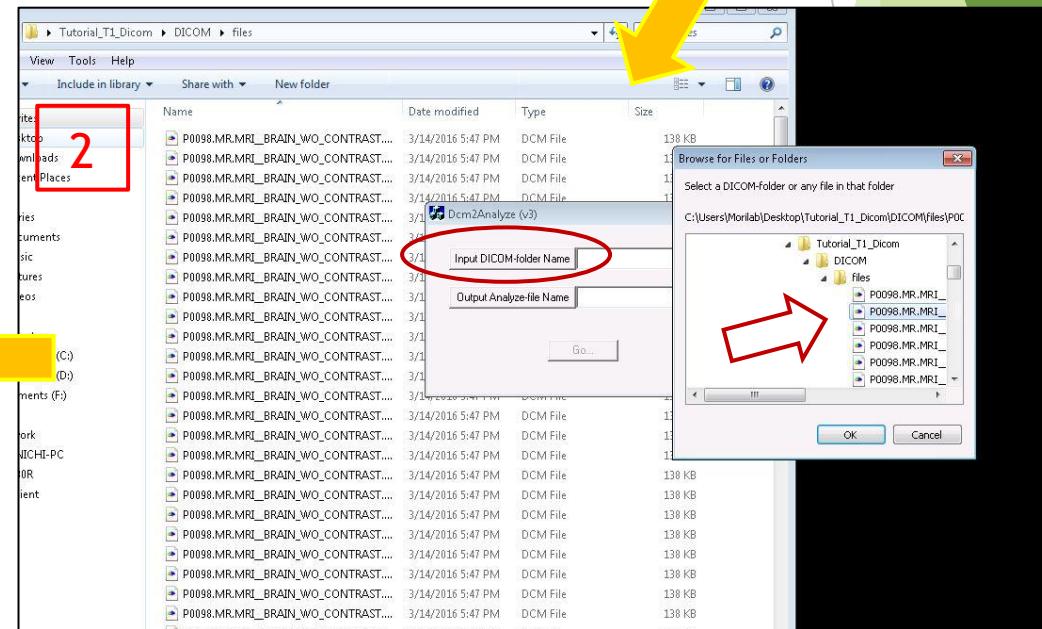
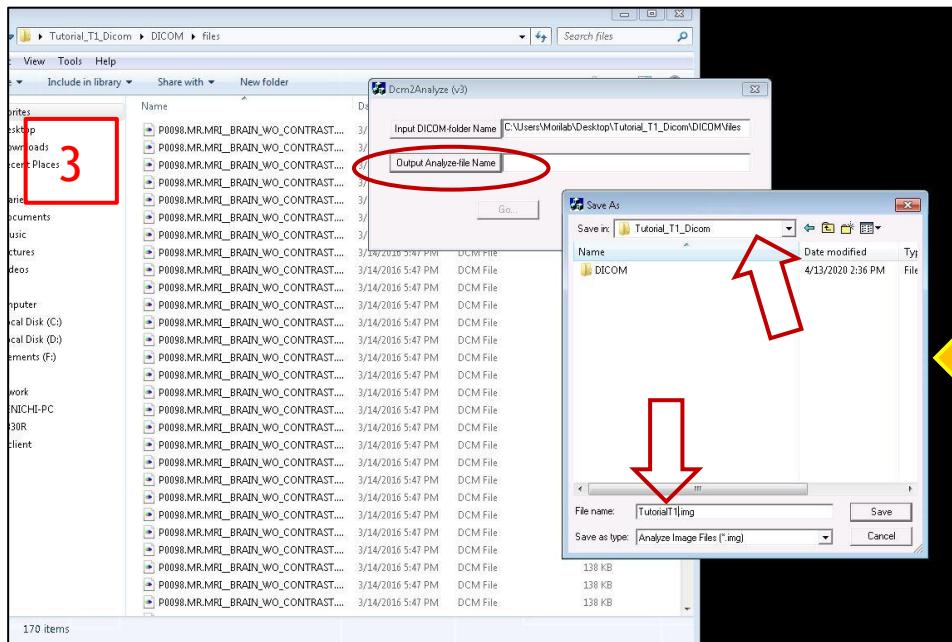
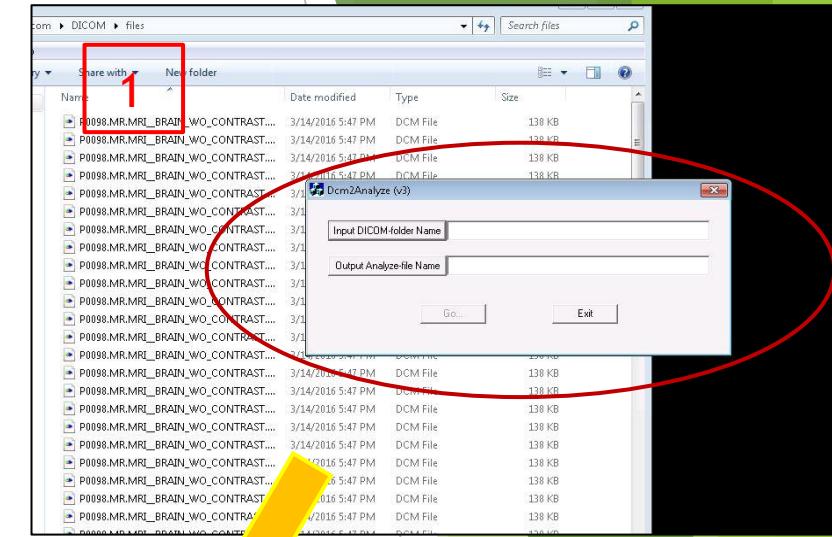
Files selected

SELECT PROCESSING SERVER

Select Image 

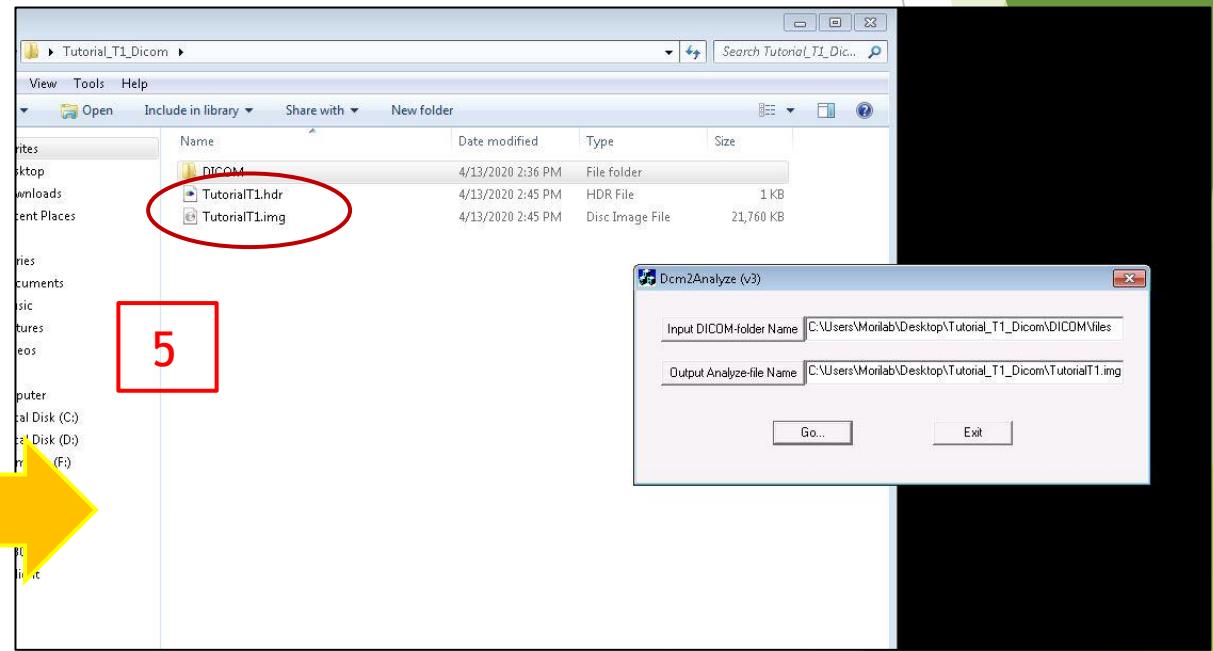
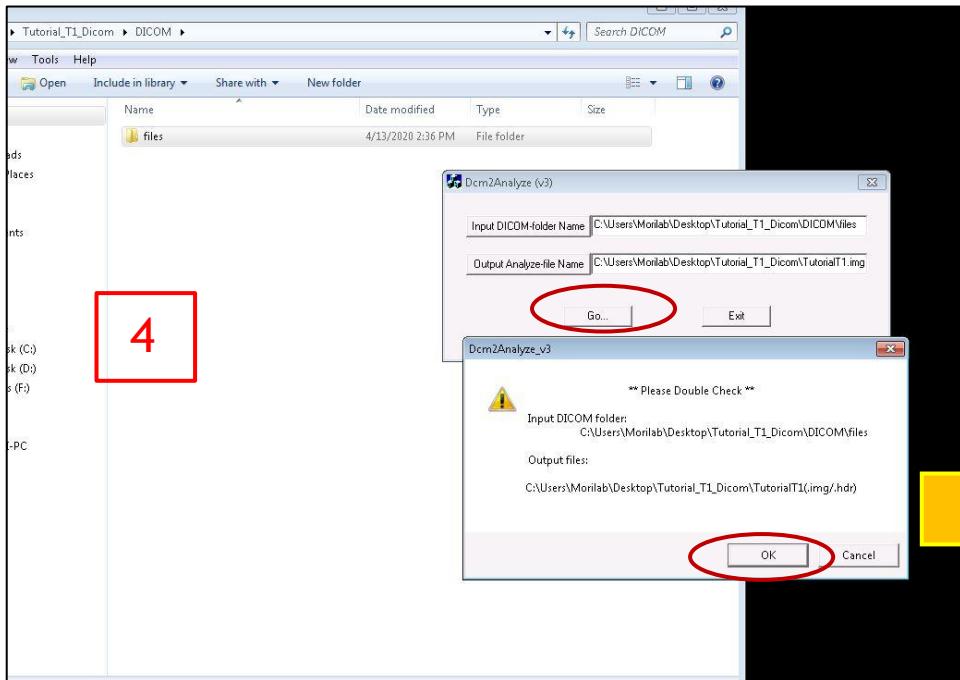
# Analyze Image - Converting Dicom to Analyze

- Once downloaded, open Dcm2Analyze converter (see image on right)
- Click on “Input DICOM-folder Name” and go to the dicom folder you want to convert, select one of the dicom files, then click OK
- Click on “Output Analyze-file Name” and go to a folder where you want to save the analyze image file. Type in a name of an image (no space) and click save.



# Analyze Image - Converting Dicom to Analyze

- 4) Click on Go button, confirm the information and click OK
- 5) You will see Analyze image (.img/.hdr) in the specified location



# Analyze Image - RoiEditor

- ▶ Once you have an Analyze image, you will need to know its slice type to run T1 pipeline
- ▶ Confirm its slice type using our RoiEditor software
  - ❖ This software is also used to inspect the output images of T1 pipeline
- ▶ Download RoiEditor from the following website. You will need to register first to download.

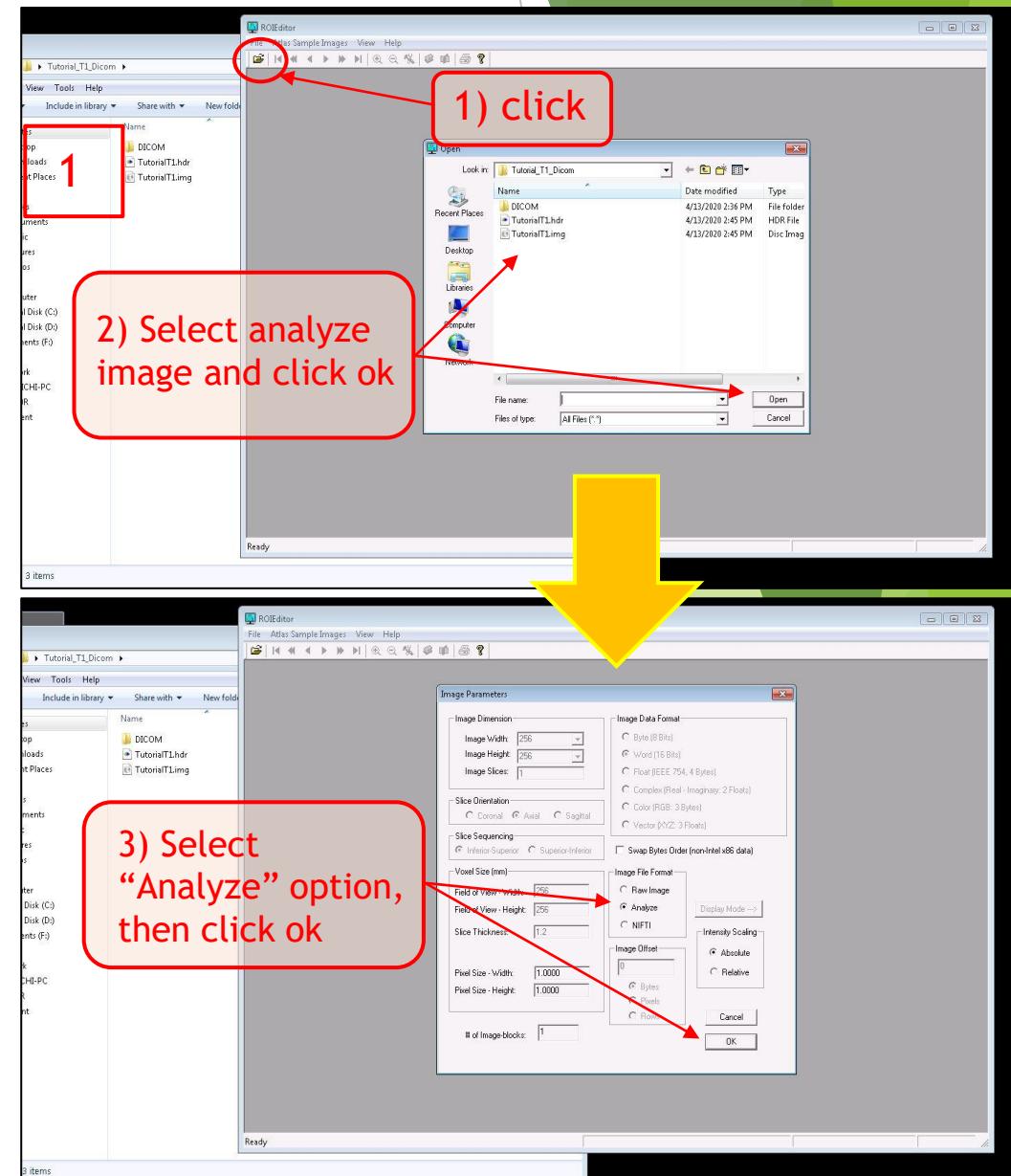
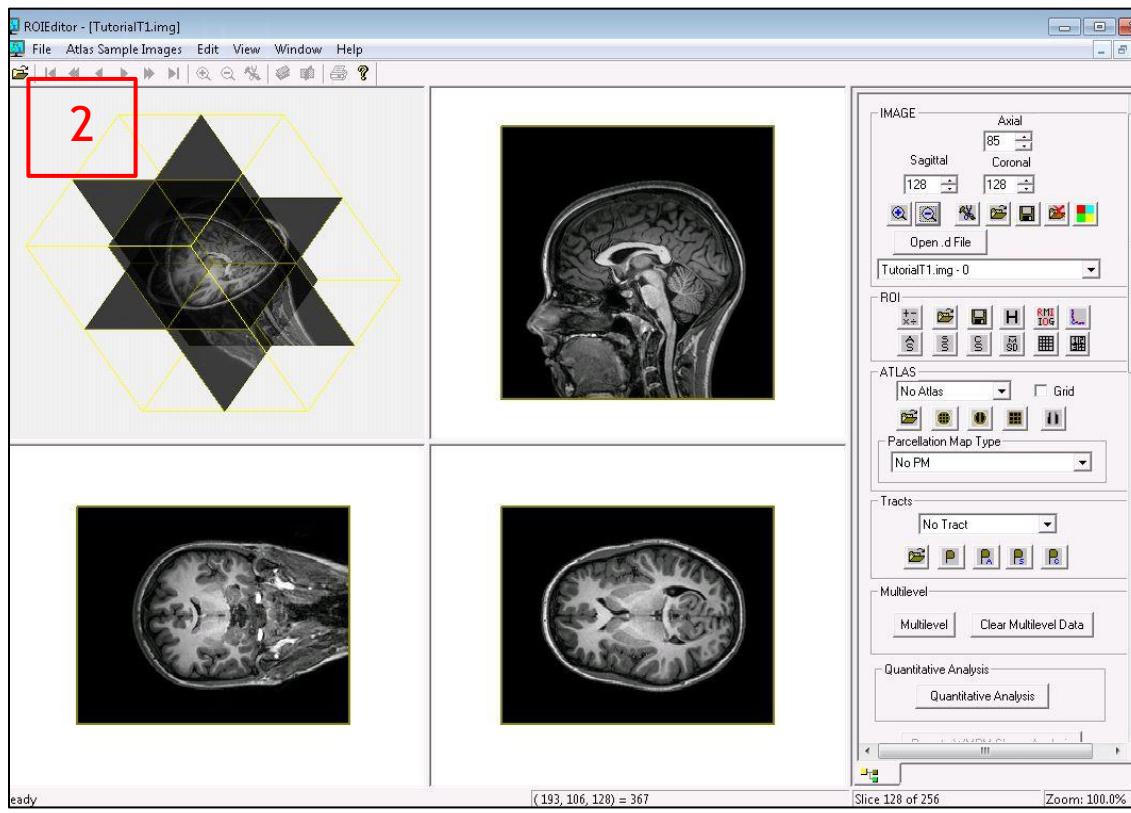
<https://www.mristudio.org/installation.html>

The screenshot shows the MRI Studio website with a red arrow pointing to the "Registration" dropdown menu. A red circle highlights the "ROIEditor-latest-x86.exe" link in the "Software Binaries" section of the download page.

Software Binaries	Description
DTIStudio_latest-x86.exe	Latest 32 bit version of DTI Studio
DTIStudio_latest-x64.exe	Latest x64 bit version of DTI Studio
DiffeoMap-latest-x86.exe	Latest 32 bit version of DiffeoMap
DiffeoMap-latest-x64.exe	Latest 64 bit version of DiffeoMap
<b>ROIEditor-latest-x86.exe</b>	Latest 32 bit version of ROIEditor
ROIEditor-latest-x64.exe	Latest x64 bit version of ROIEditor
DTI3DMRI.zip	32 bit version
vcredist_x86.exe	Microsoft Visual Studio Redistribution package need for 32 bit applications
vcredist_x64.exe	Microsoft Visual Studio Redistribution package need for x64 applications
CAWorks	Computational Anatomy Works (CAWorks) for Windows, Linux and Mac
<a href="https://www.mristudio.org/download/binaries">https://www.mristudio.org/download/binaries</a>	Download directory of all the binaries
MD5SUM	md5sum of binaries
DTI Data	DTI Data

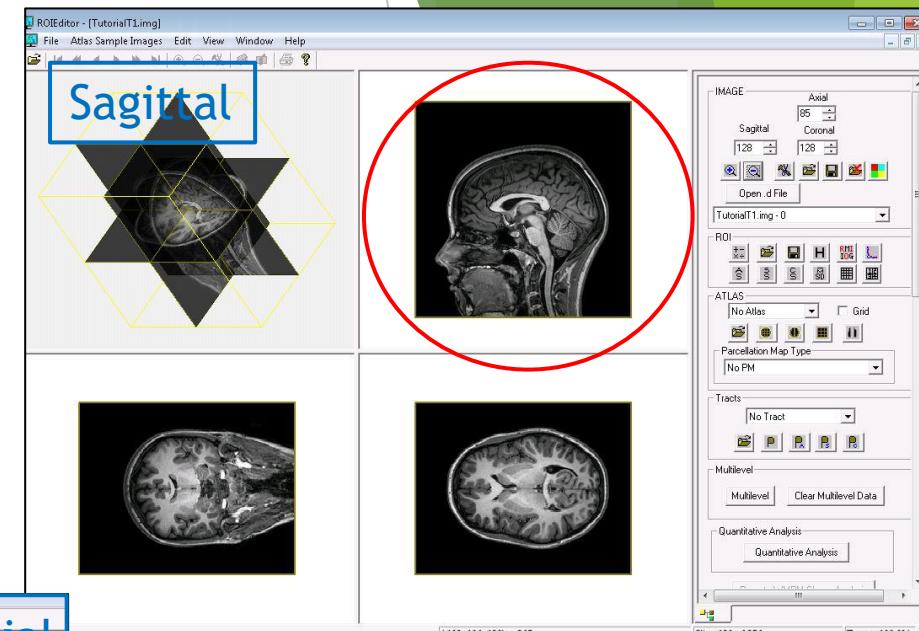
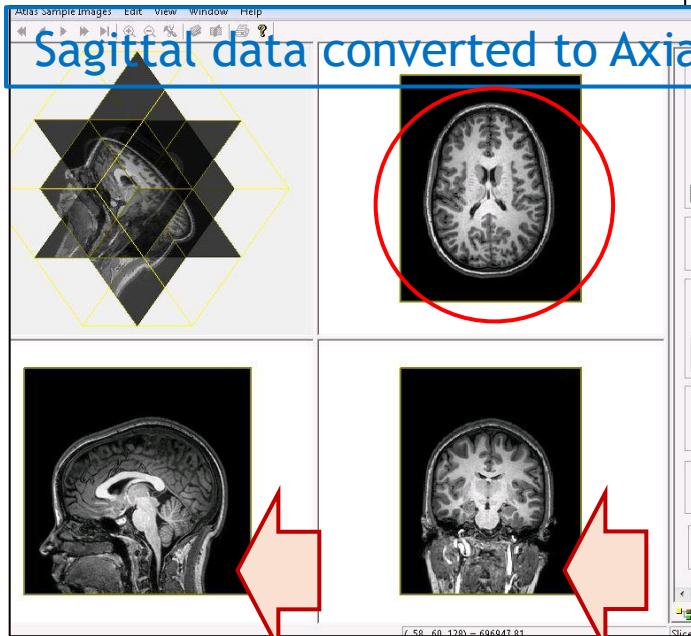
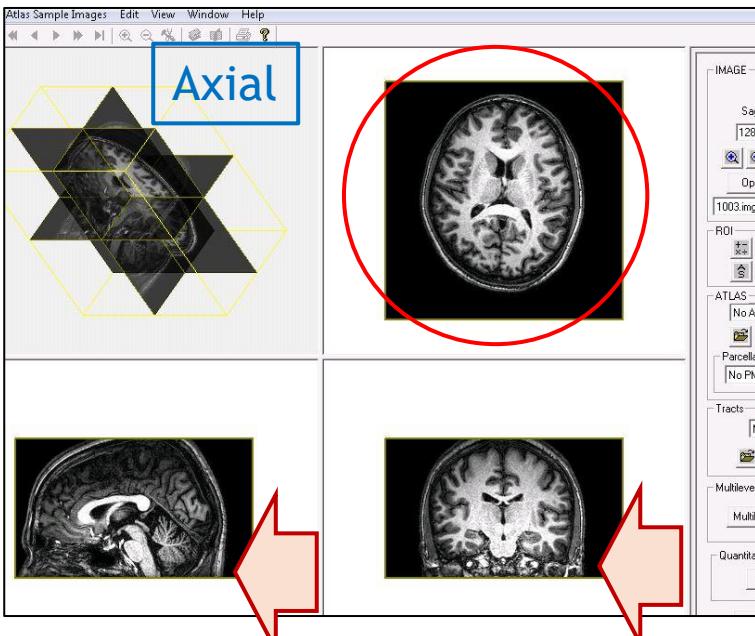
# Analyze Image - Confirming Slice Type

- 1) Once downloaded, open RoiEditor and load Analyze image (see image on right)
- 2) Loaded Analyze image would look something like this ↓



# Analyze Image - Confirming Slice Type

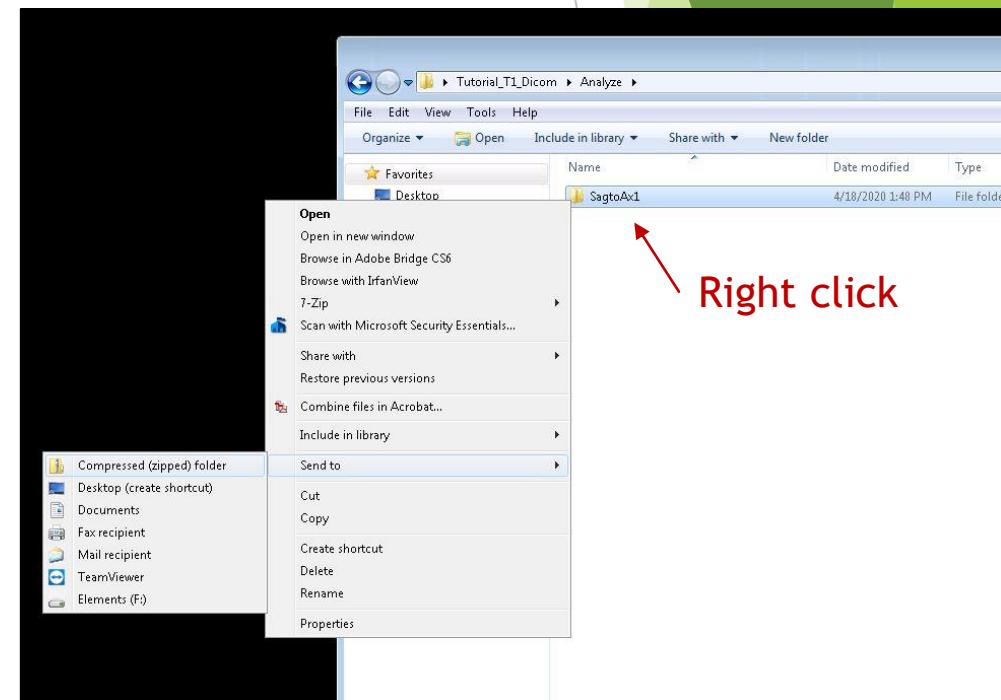
- Take a look at the image on right. The top right box (marked with red circle) shows a Sagittal image. When you see a Sagittal image on the top right box, the slice type is **Sagittal**.
- When you see an Axial image on the top right box like in the images below, you would need to determine if the slice type is an “**Axial**” or “**Sagittal data converted to Axial**” image.
- Axial** images usually do not contain much of parts below brain (see red arrows)
- Sagittal data converted to Axial** images include neck within the image (see red arrows)



\*When you have Coronal image, you would need to convert it to Axial image and confirm R-L orientation using another visualization program you can trust.

# Preparing Zip file

- ▶ Once you confirm the image slice type, sort analyze images into one folder
- ▶ A folder you prepare should only include analyze images that have the same slice type and are in similar age range
  - ❖ If you have multiple data with various slice types or age ranges, use multiple folders
  - ❖ Age ranges are grouped around 4-8yrs, 8-19yrs, 20-50yrs, and 50-90yrs
- ▶ Maximum you can put in a folder is 10 images
- ▶ Once you place Analyze images in a folder, right click on the folder and select “Send to” >> “Compressed (zipped) folder” (see image on right)
- ▶ Do not include any space in the zip folder name
- ▶ Also, the size of the total data matters. Decrease the number of images in a folder if the size of the zip file becomes greater than 120,000 KB.



# Uploading Zip file

- ▶ Once you prepare a zip file, upload it on MriCloud
  - ❖ <https://braingps.mricloud.org> >> Sign in >> Top menu bar: Segmentation >> T1-MultiAtlas Batch >> “+ .zip”
- ▶ On this page, you will be selecting Slice type and Atlas version
- ▶ Go ahead and select slice type of the uploaded zip file
- ▶ Atlas version will be explained on the next page

To start over, refresh the page

Put your .hdr and .img files in one zip file and upload (don't put more than 10 subjects one zip file)

+ .zip Click and select zip file

Files selected

SELECT PROCESSING SERVER

Computational Anatomy Science Gateway

SELECT SLICE TYPE

Sagittal

SELECT ATLAS + VERSION HISTORY:

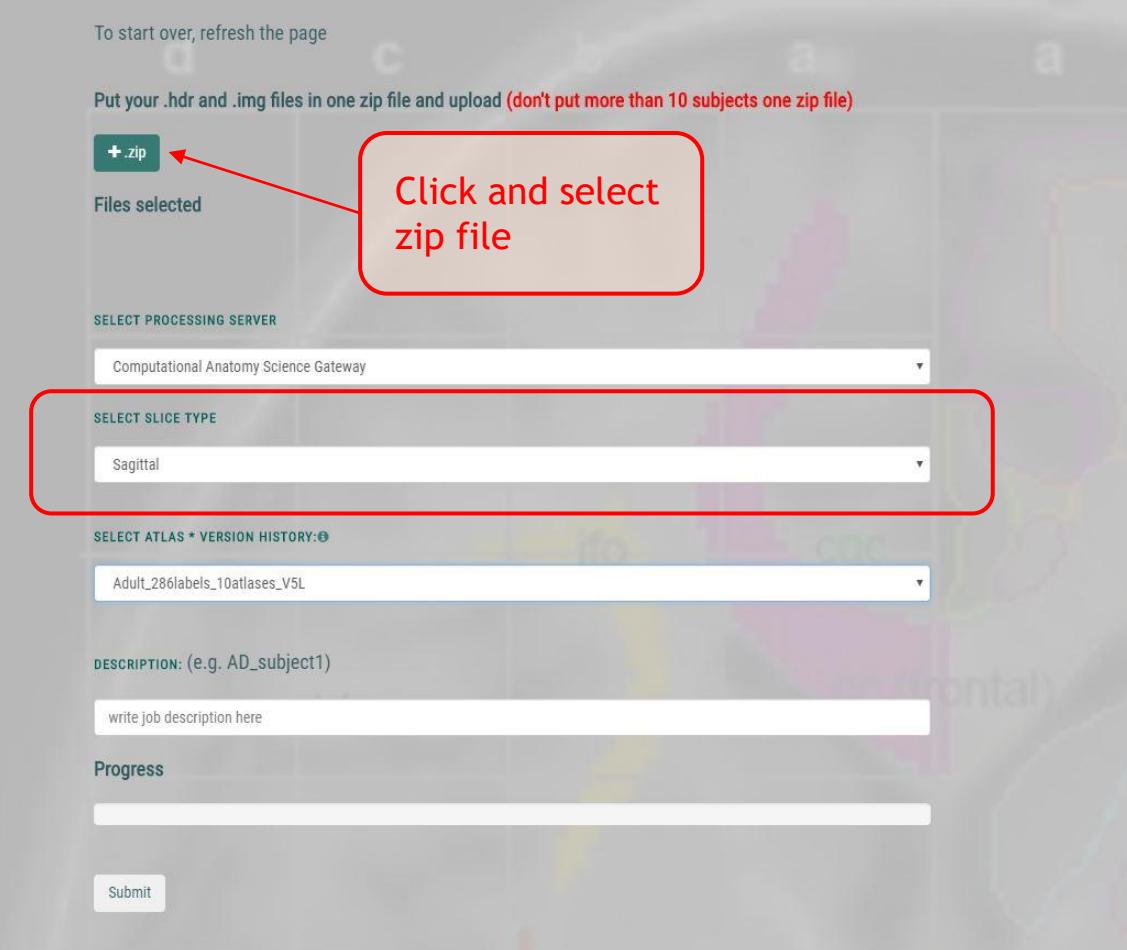
Adult\_286labels\_10atlases\_V5L

DESCRIPTION: (e.g. AD\_subject1)

write job description here

Progress

Submit



# Atlas Version

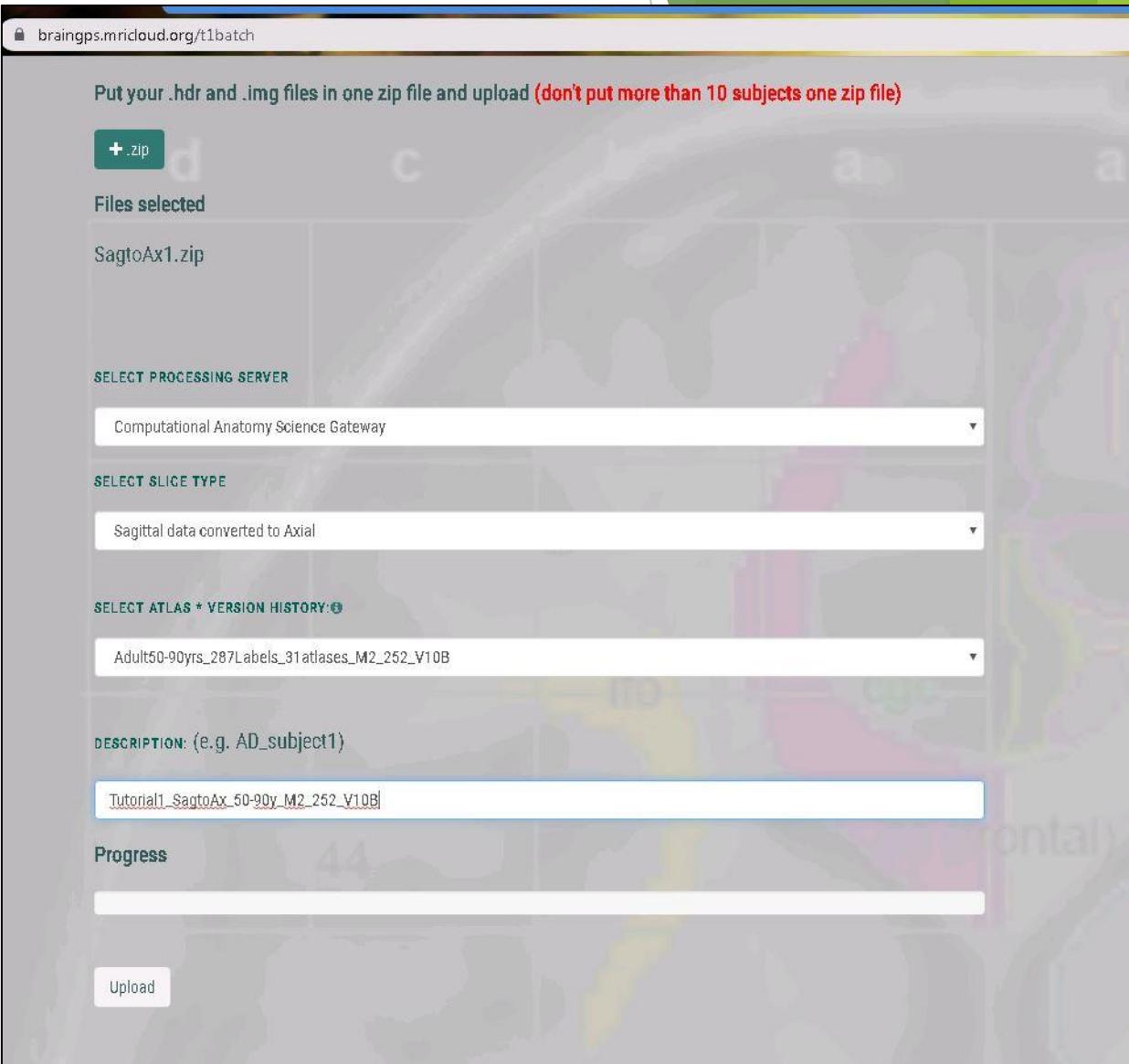
- ▶ Atlases are separated into age groups
  - ❖ Adult50-90y
  - ❖ Adult22-90y
  - ❖ Pediatric8-19y
  - ❖ Pediatric4-8y
  - ❖ Pediatric4-8y\_NoFatSat
- ▶ Each Atlas version contain different numbers of region of interest (ROI), or labels
  - ❖ V7 have 289 labels, V9 have 283 labels, V10 have 287 labels, etc.
- ▶ Newer atlas version have the more updated segmentation
  - ❖ In general, use the newer version
  - ❖ Be consistent with the version used so that the study results are comparable (i.e. the same number of labels)
- ▶ Each Atlas version have 3 different options like in the example shown below:
  - ❖ Adult22-50yrs\_287Labels\_26atlases\_V10B
  - ❖ Adult22-50yrs\_287Labels\_26atlases\_M2\_V10B
  - ❖ Adult22-50yrs\_287Labels\_26atlases\_M2\_252\_V10B
  - Use \*\_M2\_252\_\* version (for improved AIR registration)

V7A: Addition of Roi 288 & 289 next to Putamen  
V7B: Made ERC (Roi 47 and 48) smaller  
V7C: Corrected how Roi 48 (R\_ERC) was invading the area of 46 and how it was 1.5 times larger than 47 (L\_ERC)  
V9A: Most of Basal Forebrain ROIs were combined to make the total of 283 Labels; 159+161+163+165=Roi 159, and 160+162+164+166=Roi 160  
V9B: Renewed multilevel lookup table for "BasalForebrain", Roi 87/88 to Anterior and Roi 159/160 to Posterior BasalForebrain  
V9C: Correction of the boundaries of central sulci and cingulate sulci  
V10A: Addition of 4 new ROI to the space above brain: Roi 284&285 (L&R) to anterior superior space, Roi 286&287 (L&R) to posterior superior space  
V10B: Correction of Roi 254, deleted from cortex and added to dura

V5: 286Labels  
V6: 287Labels  
V7: 289Labels  
V9: 283Labels  
V10: 287Labels

# Running T1 pipeline

- ▶ Select appropriate Atlas version for your images
- ▶ Description section (optional) can be used to note what options you chose (slice type, age-range of the images, atlas version, etc.) for your zip file
- ▶ Double check your selected options, then Submit
  
- ▶ If you have other zip files to upload, refresh the page and start over



braingps.mridcloud.org/t1batch

Put your .hdr and .img files in one zip file and upload (don't put more than 10 subjects one zip file)

+ .zip

Files selected  
SagtoAx1.zip

SELECT PROCESSING SERVER  
Computational Anatomy Science Gateway

SELECT SLICE TYPE  
Sagittal data converted to Axial

SELECT ATLAS \* VERSION HISTORY: ⓘ  
Adult50-90yrs\_287Labels\_31atlases\_M2\_252\_V10B

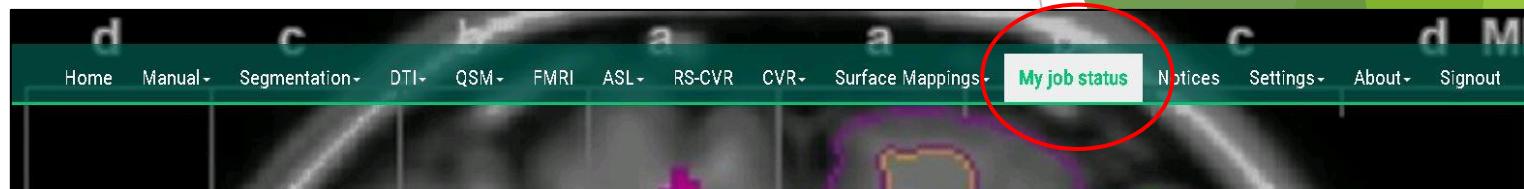
DESCRIPTION: (e.g. AD\_subject1)  
Tutorial1\_SagtoAx\_50-90y\_M2\_252\_V10B

Progress

Upload

# Download Result

- ▶ Click on “My job status” at the top menu bar
- ▶ Your submitted job would be completed within a few days
- ▶ Download result when it is available



The screenshot shows the software's main menu bar with various analysis tools like Home, Manual, Segmentation, DTI, QSM, FMRI, ASL, RS-CVR, CVR, and Surface Mappings. The "My job status" option is highlighted with a red circle. Below the menu, a "Job Status" section displays a warning about limited storage space and monthly job quotas. A table titled "LIST OF YOUR JOBS" shows one entry with ID 37950, submission date 2020-04-27 18:36:09 UTC, job type T1MultiAtlasBatch, and description Tutorial1\_SagtoAx\_50-90y\_M2\_252\_V10B. The status is listed as "submitted" and the action is "please check back later".

ID	md5sum (if any)	Submission Date	Job Type	Description	Status	Action	Delete
37950	109c30d56910fcbb2276c5487bbcf10d2	2020-04-27 18:36:09 UTC	T1MultiAtlasBatch	Tutorial1_SagtoAx_50-90y_M2_252_V10B	submitted	please check back later	<button>Delete</button>

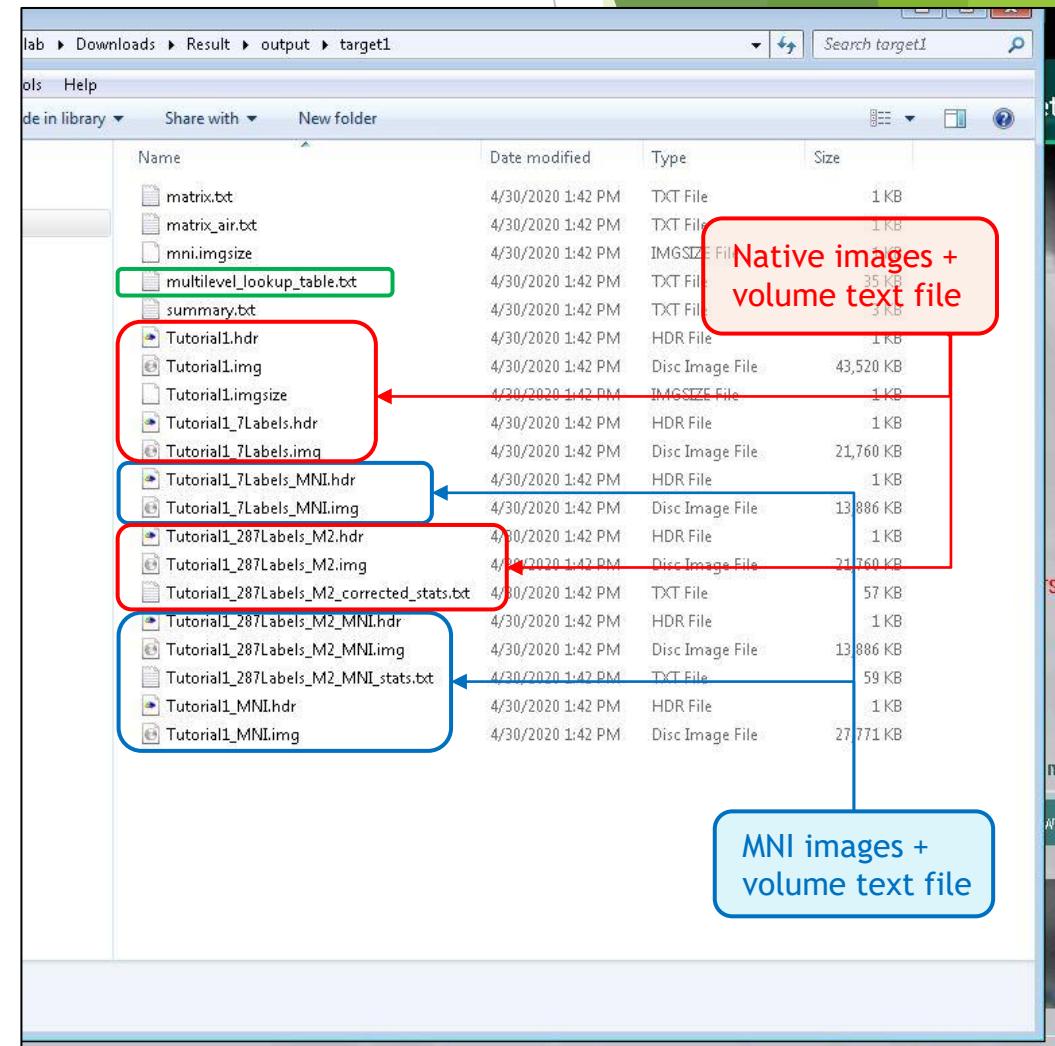


The screenshot shows the same software interface after the job has completed. The table now lists the job as "finished" and includes a green "Download Result" button next to the "Action" column. A large yellow arrow points to this "Download Result" button.

ID	md5sum (if any)	Submission Date	Job Type	Description	Status	Action	Delete
37950	109c30d56910fcbb2276c5487bbcf10d2	2020-04-27 18:36:09 UTC	T1MultiAtlasBatch	Tutorial1_SagtoAx_50-90y_M2_252_V10B	finished	<button>Download Result</button>	<button>Delete</button>

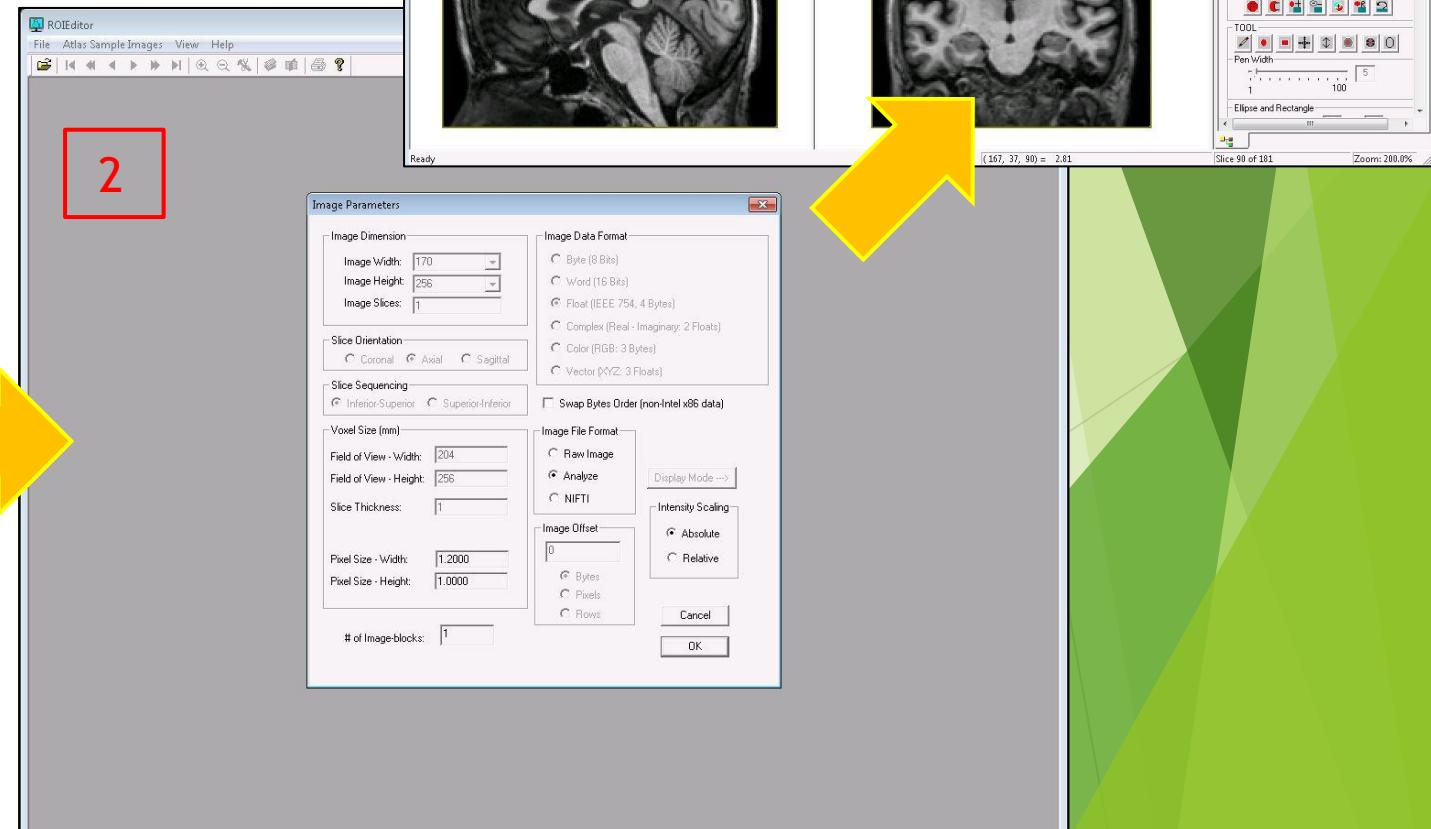
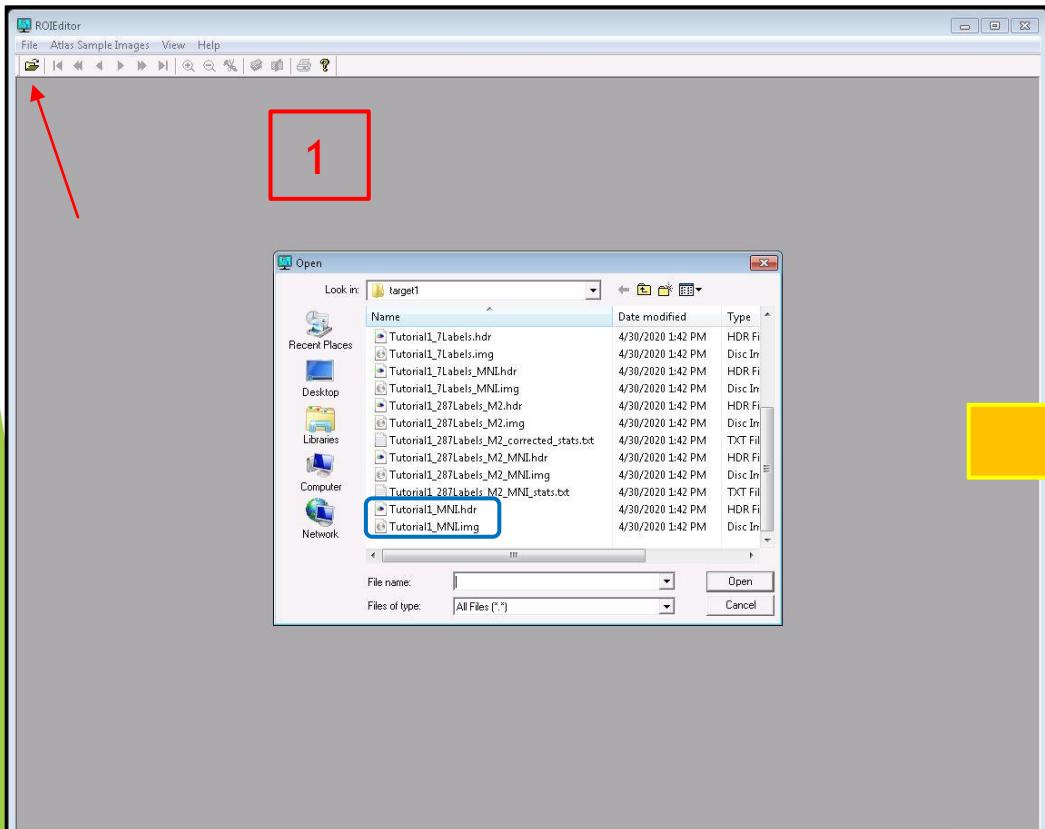
# Result

- ▶ Once downloaded, unzip the result folder
- ▶ Result folder contains the following files:
  - ▶ Native images
    - ▶ Native image (submitted Analyze image converted to Axial orientation, histogram matched, and intensity inhomogeneity corrected; matrix size remains the same as the original, submitted image)
    - ▶ Native 7 Labels image
    - ▶ Native 280+ Labels image (# of Labels differ depending on atlas version selected)
    - ▶ Corrected stats text file (summarizes volumes of Native 280+ Labels)
  - ▶ MNI images
    - ▶ MNI image (linearly normalized to the MNI space for segmentation; The matrix size is 181x217x181 / 1 x 1 x 1 mm)
    - ▶ MNI 7 Labels image
    - ▶ MNI 280+ Labels image (# of Labels differ depending on atlas version selected)
    - ▶ MNI stats text file (summarizes volumes of MNI 280+ Labels)
  - ▶ Multilevel lookup table (structure look-up table in text file)



# Inspecting Result Images

- ▶ All output images are in Analyze format
- 1) Open RoiEditor, click on folder icon on top left, click on MNI or Native image file you want to inspect, then click ok
  - ❖ Native: SubjectName.**img** or MNI: SubjectName\_**MNI.img**
- 2) Select Analyze option and click ok
- 3) Once image is opened, load ROI image:
  - ❖ Click on folder icon under “ROI” (see red circle) >> Select Analyze >> Click ok

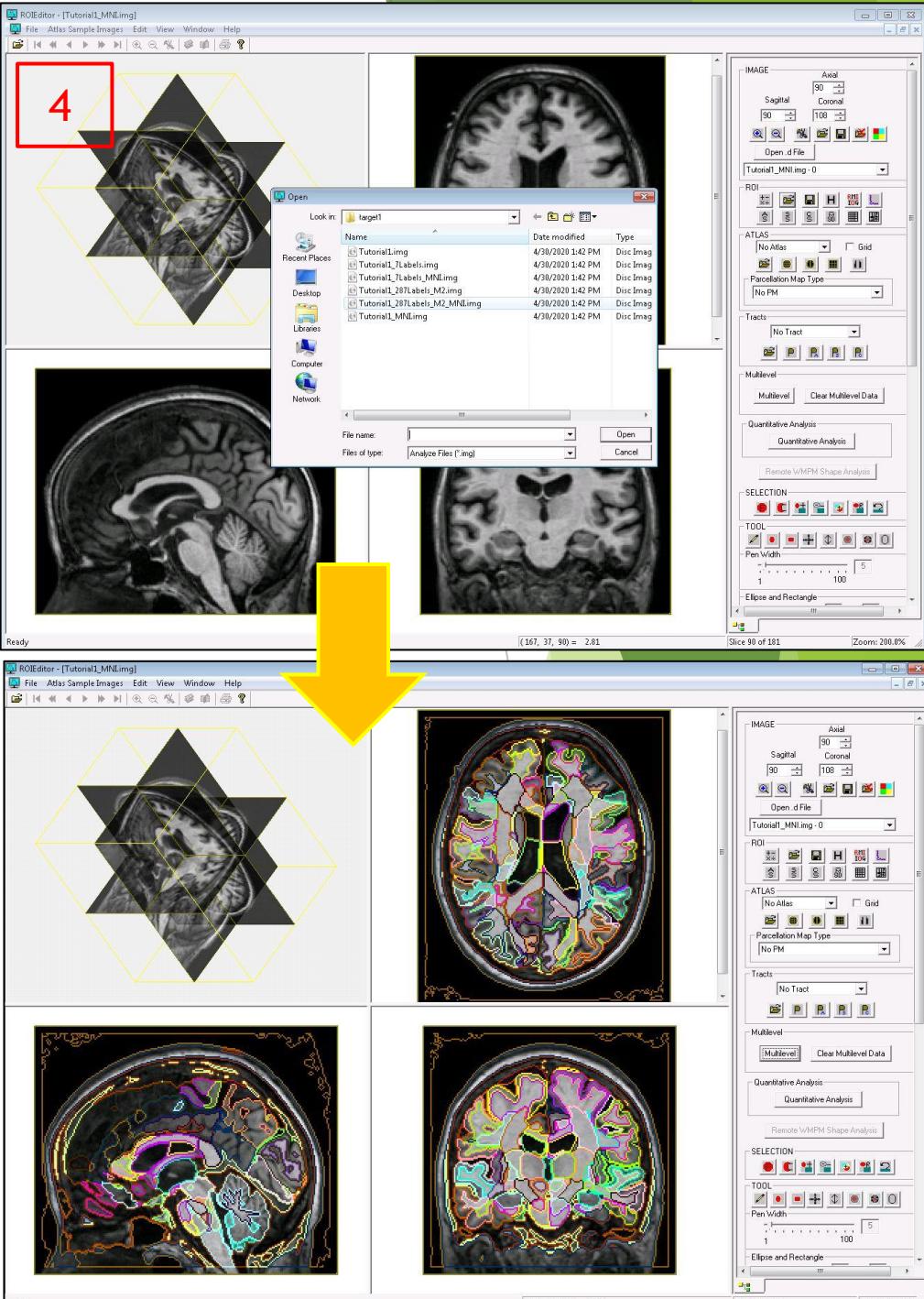
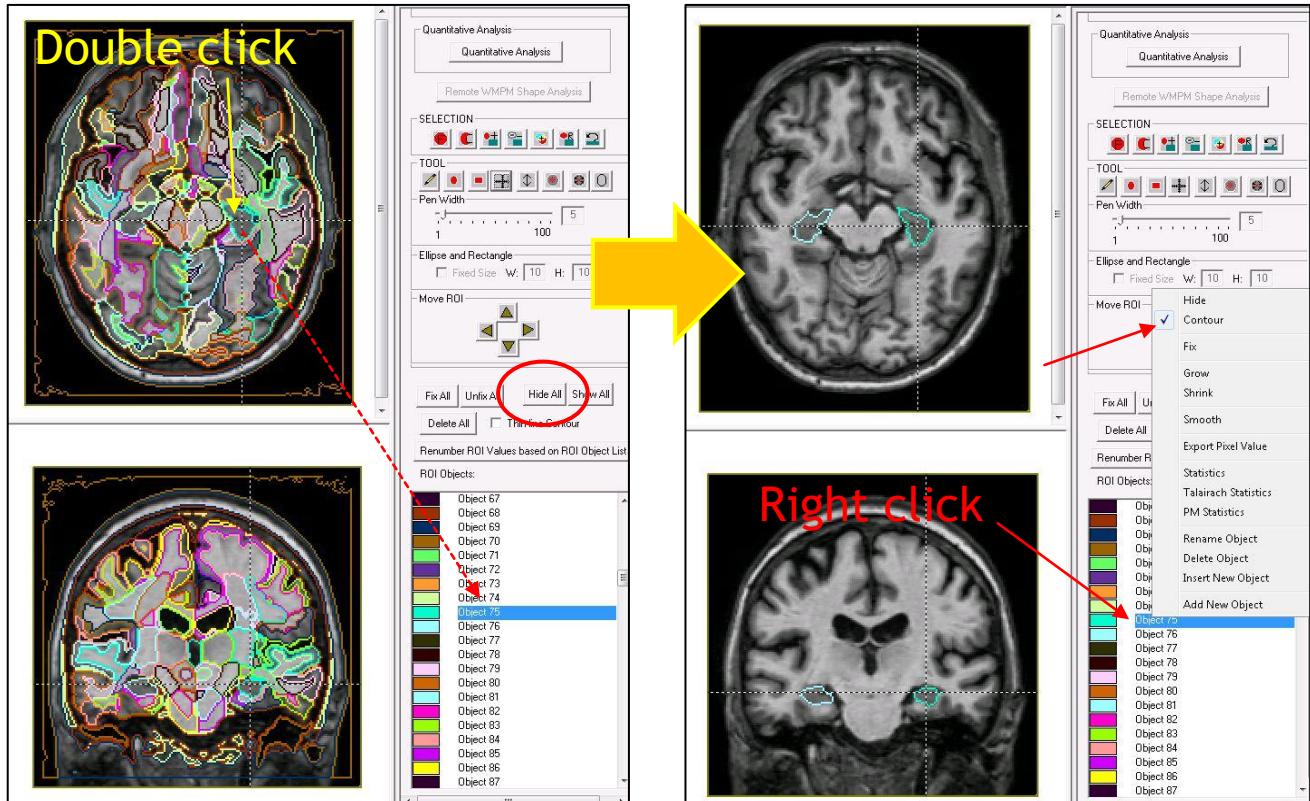


# Inspecting Result Images

4) Select 280+ Label image, and hit ok (see image on right)

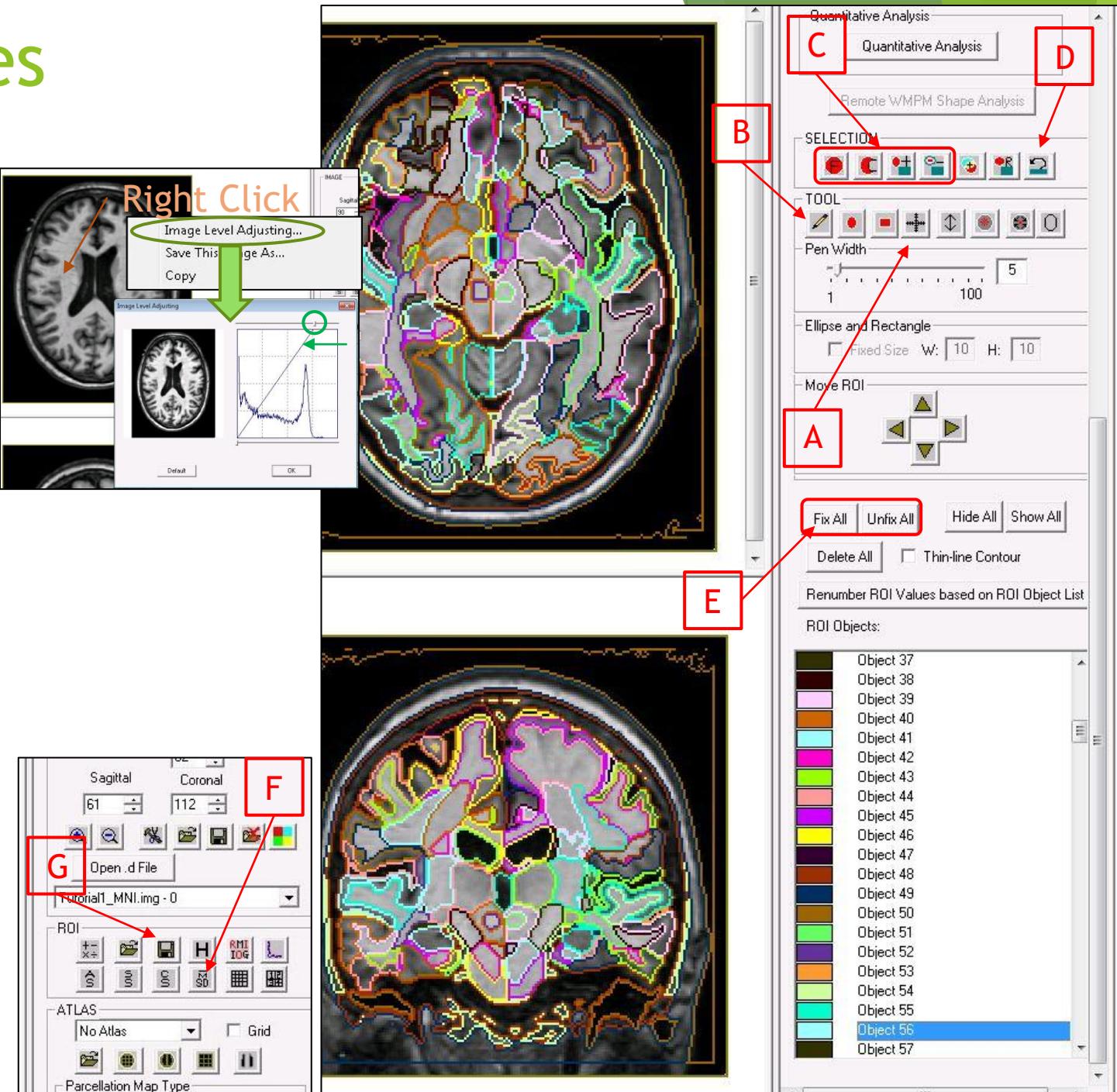
- Native: SubjectName\_280+Labels\_M2.img
- MNI: SubjectName\_280+Labels\_M2\_MNI.img

- Double clicking on any label seen on segmentation map will show you its Object # on the bottom right screen (see image below)
- To visualize only the labels of your interest, double click on the color-labeled anatomical structure of interest, check the Object #'s, click on “Hide All” (see red circle), right click on the Object #'s you want to visualize, then click on “Contour”



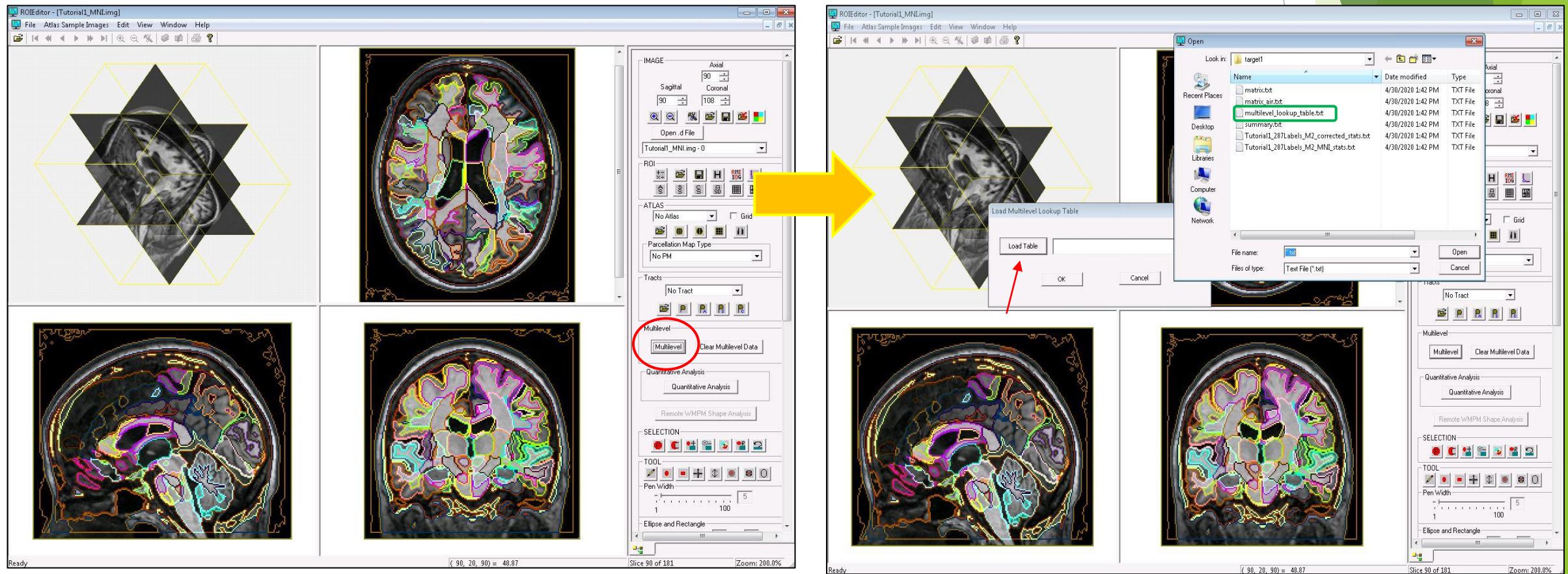
# Inspecting Result Images

- ▶ This slide will explain other basic features of RoiEditor
  - ▶ Right clicking anywhere on image allows you to adjust image brightness (see image on right)
- A. Slice Marker: aligns all 3 slices (Axial, Sagittal, and Coronal screen) to where you double click on image
- B. Drawing pen: allows you to draw marks on image to manually modify ROI
- C. Starting from left, \*() is a shortcut key
  - Fill(f): fills the mark made by pen
  - Clear(c): clears any marking made
  - Add(a): adds selected ROI to the marking
  - Subtract(s): subtracts selected ROI from the marking
- D. Undo (u): undo the previous Add or Subtract. \*Undoes only once each time
- E. Fix All/Unfix All: Fixed ROIs cannot be modified by Add/Subtract features. Right clicking on Object # allows you to fix or unfix one by one.
- F. ROI Statistics: generates list of volumes of each ROI
- G. Save: Saves modified ROI image



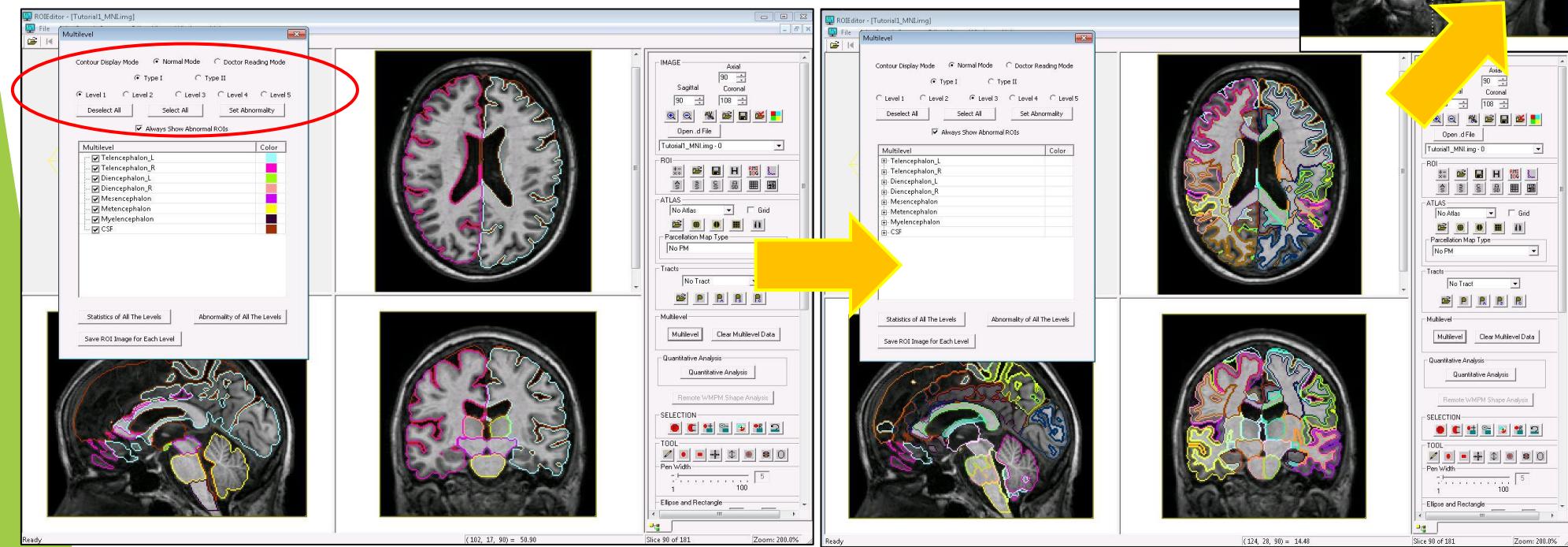
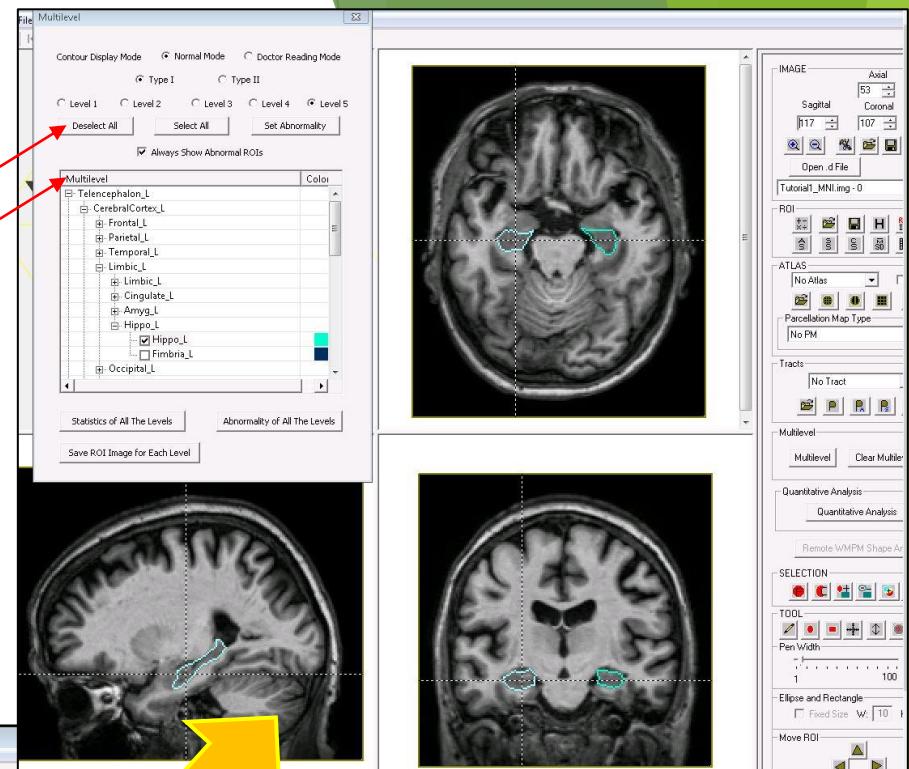
# Inspecting Result Images

- ▶ For multi-granularity analysis, load multilevel lookup table on RoiEditor
  - ❖ Click on “Multilevel” button (see red circle) >> click on “Load Table” >> select multilevel\_lookup\_table.txt >> hit ok



# Inspecting Result Images

- On multilevel lookup table screen, you can choose Type I or Type II hierarchical trees when inspecting result images (see red circle below)
  - Type1: classification widely used by anatomists
  - Type2: classification widely used in radiology
- Different granularity levels of classification can be visualized by switching Level #s (see red circle below)
- “Deselect All” the labels and select structures of interest for visualizing only the selected labels on any level (see the image on top right)
  - E.g. to visualize hippocampus, Select Level 5 and Deselect All the labels. On the Multilevel chart, click through Telencephalon\_L/R >> CerebralCortex\_L/R >> Limbic\_L/R >> Hippo\_L/R and select hippocampus.



# Inspecting Result Text Files

- ▶ Opening the Multilevel lookup table file from the result folder directly in Microsoft Excel gives you easier, aligned view
- ▶ It lists the ROI abbreviations and classifications of each ROI belonging to bigger structures
- ▶ It provides 5 granularity levels in 2 different types of anatomical classifications
  - ▶ First column (Column A) is the ROI # that matches the Object #, or Label #, seen on RoiEditor. For example, ROI #75 is labeling left hippocampus.



A	B	C	D	E	F	G	H	I	J	K	L	M
1	Type1-L5	Type1-L4	Type1-L3	Type1-L2	Type1-L1	Type2-L5	Type2-L4	Type2-L3	Type2-L2	Type2-L1		
68	67 dorsal_ACC_L	Cingulate_L	Limbic_L	CerebralCortex_L	Telencephalon_L	dorsal_ACC_L	Cingulate_L	Limbic_L	Hemisphere_L	Hemisphere_L		
69	68 dorsal_ACC_R	Cingulate_R	Limbic_R	CerebralCortex_R	Telencephalon_R	dorsal_ACC_R	Cingulate_R	Limbic_R	Hemisphere_R	Hemisphere_R		
70	69 PCC_L	Cingulate_L	Limbic_L	CerebralCortex_L	Telencephalon_L	PCC_L	Cingulate_L	Limbic_L	Hemisphere_L	Hemisphere_L		
71	70 PCC_R	Cingulate_R	Limbic_R	CerebralCortex_R	Telencephalon_R	PCC_R	Cingulate_R	Limbic_R	Hemisphere_R	Hemisphere_R		
72	71 Insula_L	Insula_L	Insula_L	CerebralCortex_L	Telencephalon_L	Insula_L	Insula_L	Insula_L	Hemisphere_L	Hemisphere_L		
73	72 Insula_R	Insula_R	Insula_R	CerebralCortex_R	Telencephalon_R	Insula_R	Insula_R	Insula_R	Hemisphere_R	Hemisphere_R		
74	73 Amyg_L	Amyg_L	Limbic_L	CerebralNucli_L	Telencephalon_L	Amyg_L	Limbic_L	Limbic_L	CerebralNucli_L	Hemisphere_L		
75	74 Amyg_R	Amyg_R	Limbic_R	CerebralNucli_R	Telencephalon_R	Amyg_R	Limbic_R	Limbic_R	CerebralNucli_R	Hemisphere_R		
76	75 Hippo_L	Hippo_L	Limbic_L	CerebralCortex_L	Telencephalon_L	Hippo_L	Limbic_L	Limbic_L	Hemisphere_L	Hemisphere_L		
77	76 Hippo_R	Hippo_R	Limbic_R	CerebralCortex_R	Telencephalon_R	Hippo_R	Limbic_R	Limbic_R	Hemisphere_R	Hemisphere_R		
78	77 Caud_L	Caud_L	BasalGang_L	CerebralNucli_L	Telencephalon_L	Caud_L	Striatum_L	BasalGang_L	CerebralNucli_L	Hemisphere_L		
79	78 Caud_R	Caud_R	BasalGang_R	CerebralNucli_R	Telencephalon_R	Caud_R	Striatum_R	BasalGang_R	CerebralNucli_R	Hemisphere_R		
80	79 Put_L	Put_L	BasalGang_L	CerebralNucli_L	Telencephalon_L	Put_L	Striatum_L	BasalGang_L	CerebralNucli_L	Hemisphere_L		
81	80 Put_R	Put_R	BasalGang_R	CerebralNucli_R	Telencephalon_R	Put_R	Striatum_R	BasalGang_R	CerebralNucli_R	Hemisphere_R		
82	81 GP_L	GP_L	BasalGang_L	CerebralNucli_L	Telencephalon_L	GP_L	GP_L	BasalGang_L	CerebralNucli_L	Hemisphere_L		

\*note that the first row of lookup table is one cell shifted to the left. From Column B, each column lists Lv 5, Lv 4, Lv 3, Lv 2, Lv 1, Lv 5', Lv 4', Lv 3', Lv 2', and Lv 1' of categorized brain structures, with Lv 5 or 5' being the highest granularity level (each label itself), and Lv 1 or 1' being the lowest granularity level (the largest category of brain structure like Telencephalon or Hemisphere).

\*\*the same structure name in different level may not have the same definition

e.g. Type1 Hippo\_L (Lv4) = Hippo\_L (Lv5) + Fimbria\_L (Lv5)

# Inspecting Result Text Files

- ▶ Opening the volume text files from the result folder directly in Microsoft Excel gives you easier, aligned view
- ▶ Volume text files (\*.stats.txt) list voxel counts of each ROI label and their classified structures
- ▶ Native volume text file (SubjectID\_280+Labels\_M2\_corrected\_stats.txt):
  - ❖ Volumes of all defined structures in Native coordinates; matrix size of the Native image remains the same as the original dimension
- ▶ MNI volume text file (SubjectID\_280+Labels\_M2\_MNI\_stats.txt):
  - ❖ Volumes of all defined structures in MNI coordinates; The matrix size is normalized to 181x217x181 / 1 x 1 x 1 mm

Gray Images		Object	Pixels	Min	Max	Mean	Std
Image	Color Images						
<b>Type1-L1 Statistics</b>							
Tutorial1_MNI.img	Telencephalon_L	593531	1.0095	245.7434	152.3178	51.1631	
Tutorial1_MNI.img	Telencephalon_R	593940	4.7126	245.6281	153.1847	50.2335	
	Diencephalon_L	10849	54.5991	252.453	179.9593	25.1734	
	Diencephalon_R	11017	47.8964	252.0214	174.4596	25.9508	
	Mesencephalon	12232	80.9686	255	205.6492	22.4429	
	Metencephalon	167016	6.6362	249.4827	141.1605	46.0481	
	Myelencephalon	5738	54.7945	246.3881	194.8088	30.1972	
	CSF	179048	0.0227	188.9225	34.581	22.5521	
<b>Type1-L2 Statistics</b>							
Tutorial1_MNI.img	CerebralCortex_L	313446	1.0095	222.8821	111.9478	32.635	
Tutorial1_MNI.img	CerebralCortex_R	314171	4.7126	218.6639	113.6233	31.7941	
	CerebralNucli_L	15132	45.0504	244.8669	160.76	27.5476	
	CerebralNucli_R	15635	50.5989	243.2875	161.1351	29.1183	
	Thalamus_L	7308	58.6064	230.722	177.7273	19.6289	
	Thalamus_R	7459	59.9743	222.9525	171.8879	22.0523	
	BasalForebrain_L	3541	54.5991	252.453	184.5657	33.3896	
	BasalForebrain_R	3558	47.8964	252.0214	179.851	31.9819	
	Mesencephalon_L	6213	80.9686	255	207.5196	21.0223	
	Mesencephalon_R	6019	82.0722	252.743	203.7186	23.666	
	Metencephalon_R	84774	7.4009	246.0612	139.6281	46.7459	
	Metencephalon_L	82242	6.6362	249.4827	142.74	45.2633	
	Myelencephalon_L	2761	54.7945	240.7294	190.8714	31.6497	
	Myelencephalon_R	2977	71.5549	246.3881	198.4606	28.2992	
	WhiteMatter_L	264953	38.5905	245.7434	199.5944	19.8359	
	WhiteMatter_R	264134	30.2852	245.6281	199.7699	19.6509	

# ROI abbreviation List

*_L: left	Cl: Clustrum Complex	GP: GLOBUS PALLIDUS
*_R: right	CP: Cerebral peduncle	Hippo: HIPPOCAMPUS
*WM: white matter	CSF: Peripheral Cerebrospinal fluid	HypoThalamus: Hypothalamus
*GM: gray matter	CST: Corticospinal tract	ICP: Inferior cerebellar peduncle
ACR: Anterior corona radiata	Cu: CUNEUS	ICP_cb: Inferior Cerebellar Peduncle cerebellar Part
AG: ANGULAR GYRUS	CuWM: CUNEUS WM	IFG_opercularis: inferior frontal gyrus pars opercularis
ALIC: Anterior limb of internal capsule	dorsal_ACC: dorsal anterior cingulate gyrus	IFG_orbitalis: inferior frontal gyrus pars orbitalis
Amyg: AMYGDALA	dorsalWM_ACC: dorsal anterior cingulate WM	IFG_triangularis: inferior frontal gyrus pars triangularis
AnsaLenticularis: Ansa lenticularis	EC: External capsule	IFO: Inferior fronto-occipital fasciculus
AnteriorCom: Anterior commissure	ECSAnterior: Extracranial space anterior	IFWM_opercularis: inferior frontal WM pars opercularis
AWM: ANGULAR WM	ECSPosterior: Extracranial space posterior	IFWM_orbitalis: inferior frontal WM pars orbitalis
BCC: Body of corpus callosum	ECCL: External capsule / claustrum	IFWM_triangularis: inferior frontal WM pars triangularis
Caud: CAUDATE NUCLEUS	ENT: ENTORHINAL AREA	III_ventricle: Third ventricle
CaudT: Caudate Tail	Fimbria: Fimbria	IV_ventricle: Fourth ventricle
CentralSul: Central Sulcus	FrontSul: Frontal Lobe Sulci	Ins: INSULAR
CerebellumGM: CEREBELLUM	FuG: FUSIFORM GYRUS	IOG: INFERIOR OCCIPITAL GYRUS
CerebellumWM: Cerebellum WM	FuWM: FUSIFORM WM	IOWM: INFERIOR OCCIPITAL WM
CGC: Cingulum (cingulate gyrus)	Fx/ST: Fornix (cres) / Stria terminalis (cannot be resolved with current resolution)	ITG: INFERIOR TEMPORAL GYRUS
CGH: Cingulum (hippocampus)	Fx: Fornix (column and body of fornix)	ITWM: INFERIOR TEMPORAL WM
CinguSul: Cingular Cortex Sulci	GCC: Genu of corpus callosum	LenticularFasc: Lenticular fasciclus

# ROI abbreviation List

LFOG: LATERAL FRONTO-ORBITAL GYRUS	MFWM: MIDDLE FRONTAL WM (posterior segment)	PLIC: Posterior limb of internal capsule
LFOWM: LATERAL FRONTO-ORBITAL WM	Midbrain: MIDBRAIN	PoCG: POSTCENTRAL GYRUS
LG: LINGUAL GYRUS	ML: Medial lemniscus	PoCWM: POSTCENTRAL WM
LV_atrium: lateral ventricle_atrium	MOG: MIDDLE OCCIPITAL GYRUS	Pons: PONS
LV_body: lateral ventricle_body	MOWM: MIDDLE OCCIPITAL WM	PrCG: PRECENTRAL GYRUS
LV_Frontal: lateral ventricle_frontal	MTG: MIDDLE TEMPORAL GYRUS	PrCWM: PRECENTRAL WM
LV_Occipital: lateral ventricle_occipital	MTG_pole: Pole of MIDDLE TEMPORAL GYRUS	PrCu: PRE-CUNEUS
LV_Temporal: lateral ventricle_temporal	MTWM: MIDDLE TEMPORAL WM	PrCuWM: PRE-CUNEUS WM
LGWM: LINGUAL WM	MTWM_pole: Pole of MIDDLE TEMPORAL WM	PTR: Posterior thalamic radiation (include optic radiation)
Mammillary: Mammillary body	Mynert: Nucleus innominata of Mynert	Put: PUTAMEN
MCP_cb: Middle Cerebellar Peduncle Cerebellar Part	NucAccumbens: Nucleus accumbens	PVWa: Periventricular White Matter frontal
MCP: Middle cerebellar peduncle	OccipitSul: Occipital Lobe Sulci	PVWp: Periventricular White Matter posterior
Medulla: MEDULLA	OlfactoryRadiation: olfactory radiation	PVWL: Periventricular White Matter posterior lateral
MFG_DPFC: Middle frontal gyrus (dorsal prefrontal cortex)	OpticTract: Optic tract	RedNc: Red Nucleus
MFG: MIDDLE FRONTAL GYRUS (posterior segment)	ParietSul: Parietal Lobe Sulci	RG: GYRUS RECTUS
MFOG: MIDDLE FRONTO-ORBITAL GYRUS	PCC: posterior cingulate gyrus	RGWM: WM RECTUS
MFOWM: MIDDLE FRONTO-ORBITAL WM	PCCWM: posterior cingulate WM	RLIC: Retrolenticular part of internal capsule
MFWM_DPFC: Middle frontal WM (dorsal prefrontal cortex)	PCR: Posterior corona radiata	rostral_ACC: rostral anterior cingulate gyrus
	PCT: Pontine crossing tract (a part of MCP)	rostralWM_ACC: rostral anterior cingulate WM
	PHG: PARAHIPPOCAMPAL GYRUS	

# ROI abbreviation List

SCC: Splenium of corpus callosum

SCP: Superior cerebellar peduncle

SCR: Superior corona radiata

SFG: SUPERIOR FRONTAL GYRUS (posterior segment)

SFG\_PFC: Superior frontal gyrus (prefrontal cortex)

SFG\_pole: superior frontal gyrus (frontal pole)

SFO: Superior fronto-occipital fasciculus (could be a part of anterior internal capsule)

SFWM: SUPERIOR FRONTAL WM (posterior segment)

SFWM\_PFC: Superior frontal WM (prefrontal cortex)

SFWM\_pole: superior frontal WM (frontal pole)

SLF: Superior longitudinal fasciculus

SMG: SUPRAMARGINAL GYRUS

SMWM: SUPRAMARGINAL WM

Snigra: Substancia Nigra

SOG: SUPERIOR OCCIPITAL GYRUS

SOWM: SUPERIOR OCCIPITAL WM

SPG: SUPERIOR PARIETAL GYRUS

SPWM: SUPERIOR PARIETAL WM

SS: Sagittal stratum (include inferior longitudinal fasciculus and inferior fronto-occipital fasciculus)

STG: SUPERIOR TEMPORAL GYRUS

STG\_pole: Pole of SUPERIOR TEMPORAL GYRUS

STWM: SUPERIOR TEMPORAL WM

STWM\_pole: Pole of SUPERIOR TEMPORAL WM

subcallosal\_ACC: subcallosal anterior cingulate gyrus

subcallosalWM\_ACC: subcallosal anterior cingulate WM

subgenual\_ACC: subgenual anterior cingulate gyrus

subgenualWM\_ACC: subgenual anterior cingulate WM

SylFrontSul: Sylvian Fissure Frontal Lobe Part

SylParieSul: Sylvian Fissure Parietal Lobe Part

SylTempSul: Sylvian Fissure Temporal Lobe Part

TAP: Tapatum

TempSul: Temporal Lobe Sulci

Thalamus: THALAMUS

UNC: Uncinate fasciculus